

***Bacillus thuringiensis* var. *morrisoni* strain PG14: nucleotide sequence of a gene encoding a 27kDa crystal protein**

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Following hybridization studies using the cloned *Bacillus thuringiensis* var. *israelensis* (Bti) 27 kDa insecticidal toxin gene and *B.t.* var. *morrisoni* strain PG14 DNA (1,2), a 1.2 kb *TaqI* fragment containing a gene encoding a 27 kDa protein has been cloned from the 74MDa plasmid of PG14. The nucleotide sequence of this gene, presented below, is highly homologous to the Bti 27 kDa toxin gene (3,4), and the gene product, expressed in *E. coli*, shows cross-reaction with anti-Bti 27 kDa toxin serum. A single base-pair difference (G replacing C, arrowed), resulting in an alanine residue in PG14 rather than the proline found in Bti, distinguishes the two. Interestingly there are no "silent" substitutions, and downstream regions, including inverted repeat sequences (underlined), are conserved. The putative Shine-Dalgarno sequence is boxed.

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100
CCCATCTTAATTAACTAAGGAGTGTTGTTATTTATGGAAAAATTTAAATCATTGTCCATTAGAAAGATATAAAAGGTAATCCATGGAAAAACCCCTCAATC
      M E N L N H C P L E D I K V N P W K T P Q S
200
AACAGCAAGGGTTATTACATTACCTGTTGAGGATCCAAATGAAATCAATAATCTTCTTTTATTAACGAAATGATAATCCGAATATATATGGCAAGCA
  T A R V I T L R V E D P N E I N N L L S I N E I D N P N Y I L Q A
300
ATTATGTTAGCAAAATGCATTTCAAAAATGCATTAGTCTCCCACTTCTACAGATTTTGGTGATGCCCTACGCTTTAGTATGGCAAAGGTTTAGAAATCGCAA
  I M L A N A F Q N A L V P P T S T D F G D A L R F S M A K G L E I A
400
ACACAATTACACCGTAGGCTGTAGTGTAGTATGTTGATCAAAATGTAACCTCAAACGAATAACCAAGTAAGTGTATGATAATAAAGTCTTAGAAGT
  N T I T P M G G V S Y V D Q N V T Q T N N Q V S V M I N K V L E V
500
GTTAAAACTGTATTAGGAGTTGCATTAAAGTGGATCTGTAATAGATCAATTAAGTGCAGCAGTTACAATAACGTTTACAATTTAAATCTCAAAAAAT
  L K T V L G V A L S G S V I D Q L T A A V T N T F T N L N T Q K N
600
GAAGCATGATTTCTGGGGCAAGGAACTGCTAATCAACAATAACACATACAATGCTCCTGTTGCAATCCAAAATGCCAAACTGGGCGGCTATGT
  E A W I F W G K E T A N Q T N Y T Y N V L P A I Q N A Q T G G V H
700
ATTGTGTACCAAGTTGGTTTGAATAAAGTATCAGCAGTAAAGGAACAAGTTTTATTTTACAATCAAGATTTCTGGAGCTACAATGTAAACATCCA
  Y C V P V G F E I K V S A V K E Q V L P F T I Q D S A S Y N V N I Q
800
ATCTTTGAAATTTGCACAACCATAGTGTAGCTCAAGTCAGTATCCAATGGCAGATCTTACTAGCGGTATTAATGGAACCCCTTAATCTTAGTAGCTATAT
  S L K F A Q P L V S S S Q Y P I A D L T S A I N G T L *
900
TTATAAATATGGTAATATCACAAGTATAAATACTTGGGTATTACCTACCAATCTTAAATATATCCAAAATCATGGGTAATCTACATTCCTCCCTTTCT
CTAAAATTGTCTTCACACATCCACATTTTTCGA
    
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